



S/N 09/730,374

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: John A. Lust et al. Examiner: Unknown
Serial No.: 09/730,374 Group Art Unit: Unknown
Filed: December 5, 2000 Docket: 150.188US2
Title: USE OF GENETICALLY ENGINEERED ANTIBODIES TO CD38 TO TREAT
MULTIPLE MYELOMA

COMMUNICATION UNDER 37 C.F.R. § 1.821

Commissioner for Patents
Washington, D.C. 20231

Sir:

A SEQUENCE LISTING, to conform the above-referenced application to the requirements of 37 C.F.R. §§ 1.821 through 1.825, is submitted herewith.

In accordance with 37 C.F.R. § 1.821(e), a copy of the above-submitted SEQUENCE LISTING in ASCII computer readable form is also submitted herewith. It is respectfully submitted that the contents of the paper version of the SEQUENCE LISTING and the computer readable form being submitted herewith are the same.

Respectfully submitted,

JOHN A. LUST ET AL.,

By their Representatives,

SCHWEGMAN, LUNDBERG, WOESSNER & KLUTH, P.A.
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Date May 7, 2001 By Janet E. Embretson
Janet E. Embretson
Reg. No. 39,665

CERTIFICATE UNDER 37 CFR 1.8: The undersigned hereby certifies that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail, in an envelope addressed to: Commissioner of Patents, Washington, D.C. 20231, on this 7th day of May, 2001.

Name Bill Schrank

Signature [Signature]



SEQUENCE LISTING

<110> Lust, John A.
Donovan, Kathleen A.

<120> USE OF GENETICALLY ENGINEERED ANTIBODIES
TO CD38 TO TREAT MULTIPLE MYELOMA

<130> 150.188US2

<140> 09/730,374

<141> 2000-12-05

<150> PCT/US99/12512

<151> 1999-06-04

<150> 60/088,277

<151> 1998-08-05

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> A nucleotide sequence encoding a single chain
variable region fragment (scFv)

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acactgggtt	cgccagtctc	caggaaaggg	tctggagtgg	ctgggagtga	tatggagagg	180
tggaagcaca	gactacaatg	cagctttcat	gtccagactg	agcatcacca	aggacaactc	240
caagagccaa	gttttcttta	aatgaacag	tctgcaagct	gatgacactg	ccatatactt	300
ctgtgccaaa	accttgatta	cgacgggcta	tgctatggac	tactggggcc	aagggaccac	360
ggtcaccgtc	tcctcaggtg	gaggcgggtc	aggcggaggt	ggctctggcg	gtggcggatc	420
ggacatcgag	ctcactcagt	ctccatcctc	cttttctgta	tctctaggag	acagagtcac	480
cattacttgc	aaggcaagtg	aggacatata	taatcggtta	gcctggtatc	agcagaaacc	540
aggaaatgct	cctaggctct	taatatctgg	tgcaaccagt	ttggaaactg	gggttccttc	600
aagattcagt	ggcagtggtg	ctggaaagga	ttacactctc	agcattacca	gtcttcagac	660
tgaagatgtt	gctacttatt	actgtcaaca	gtattggagt	actcctacgt	tcggtggagg	720
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<220>

<223> A polypeptide encoded by an open reading frame of
SEQ ID NO:1

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Ser	Ala	Ala	Leu	Thr	Ala	Pro	Val	His	Asn	Leu	His	Ser	Leu	Trp	Phe
			20					25					30		
Leu	Ile	Asn	Leu	Trp	Cys	Thr	Leu	Gly	Ser	Pro	Val	Ser	Arg	Lys	Gly
		35					40					45			
Ser	Gly	Val	Ala	Gly	Ser	Asp	Met	Glu	Arg	Trp	Lys	His	Arg	Leu	Gln
		50				55					60				
Cys	Ser	Phe	His	Val	Gln	Thr	Glu	His	His	Gln	Gly	Gln	Leu	Gln	Glu
65					70					75					80
Pro	Ser	Phe	Leu	Asn	Glu	Gln	Ser	Ala	Ser	His	Cys	His	Ile	Leu	Leu
				85					90					95	
Cys	Gln	Asn	Leu	Asp	Tyr	Asp	Gly	Leu	Cys	Tyr	Gly	Leu	Leu	Gly	Pro
		100						105					110		
Arg	Asp	His	Gly	His	Arg	Leu	Leu	Arg	Trp	Arg	Arg	Phe	Arg	Arg	Arg
		115					120					125			
Trp	Leu	Trp	Arg	Trp	Arg	Ile	Gly	His	Arg	Ala	His	Ser	Val	Ser	Ile
		130					135					140			
Leu	Leu	Phe	Cys	Ile	Ser	Arg	Arg	Gln	Ser	His	His	Tyr	Leu	Gln	Gly
145					150					155					160
Lys	Gly	His	Ile	Ser	Val	Ser	Leu	Val	Ser	Ala	Glu	Thr	Arg	Lys	Cys
			165						170					175	
Ser	Ala	Leu	Asn	Ile	Trp	Cys	Asn	Gln	Phe	Gly	Asn	Trp	Gly	Ser	Phe
		180					185						190		
Lys	Ile	Gln	Trp	Gln	Trp	Ile	Trp	Lys	Gly	Leu	His	Ser	Gln	His	Tyr
		195					200					205			
Gln	Ser	Ser	Asp	Arg	Cys	Cys	Tyr	Leu	Leu	Leu	Ser	Thr	Val	Leu	Glu
		210				215					220				
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<212> PRT

<213> Artificial Sequence

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SEQ ID NO:1

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Leu	Val	Gln	Pro	Ser	Gln	Arg	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly
		20						25					30		
Phe	Ser	Leu	Ile	Ser	Tyr	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly
		35					40					45			
Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Arg	Gly	Gly	Ser	Thr	Asp
		50				55					60				
Tyr	Asn	Ala	Ala	Phe	Met	Ser	Arg	Leu	Ser	Ile	Thr	Lys	Asp	Asn	Ser
65					70					75					80
Lys	Ser	Gln	Val	Phe	Phe	Lys	Met	Asn	Ser	Leu	Gln	Ala	Asp	Asp	Thr
			85						90					95	
Ala	Ile	Tyr	Phe	Cys	Ala	Lys	Thr	Leu	Ile	Thr	Thr	Gly	Tyr	Ala	Met

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<210> 4
<211> 239
<212> PRT
<213> Artificial Sequence

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Alt.

